

#2

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/843,377

DATE: 05/14/2001

TIME: 09:23:55

Input Set : A:\RTS-0235 Sequence Listing.txt

Output Set: N:\CRF3\05142001\I843377.raw

ENTERED

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6 <110> APPLICANT: C. Frank Bennett
7   Andrew T. Watt
9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF INTERFERON GAMMA RECEPTOR 2 EXPRESSION
11 <130> FILE REFERENCE: RTS-0235
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/843,377
C--> 13 <141> CURRENT FILING DATE: 2001-04-26
13 <160> NUMBER OF SEQ ID NOS: 89
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 20
18 <212> TYPE: DNA
19 <213> ORGANISM: Artificial Sequence
21 <220> FEATURE:
23 <223> OTHER INFORMATION: Antisense Oligonucleotide
25 <400> SEQUENCE: 1
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29 <210> SEQ ID NO: 2
30 <211> LENGTH: 20
31 <212> TYPE: DNA
32 <213> ORGANISM: Artificial Sequence
34 <220> FEATURE:
36 <223> OTHER INFORMATION: Antisense Oligonucleotide
38 <400> SEQUENCE: 2
39 atgcattctg cccccaagga                               20
42 <210> SEQ ID NO: 3
43 <211> LENGTH: 2214
44 <212> TYPE: DNA
45 <213> ORGANISM: Homo sapiens
47 <220> FEATURE:
48 <221> NAME/KEY: CDS
49 <222> LOCATION: (649)...(1662)
51 <400> SEQUENCE: 3
52 gttgactgga ggcggaggtt gcagtgagcc gagatcgccc cactgcactc cagcctggtg      60
54 actccgtctc aaaaaaaagg ggaggggggc gggggagagt tgaaagctta atatgtactt      120
56 tgggggctat taaagcaaac atttcgacta aaggggagaa tcctcgaatt gtgcgatcaa      180
58 gcacccgaga ggagagtgtg ggggggtcag gaggggtggg ggctccaggg aacgcccggg      240
60 ggcctgggoc ggggtctcgc ggggcccttc cggaaggatc gcggcccccg aaggtggggc      300
62 tcccgcgggg ctccagtctc caggacgttc cgggaggctc cgcgtctctg gaggccggct      360
64 gcgtggggtc cccgcgctgc agccgcagag gccccccagg gccgcgggtc ccggagcggg      420
66 aaagtccgcg gcggggggcg tggcctcggg ggcgggacgg ggcgggggcg ggggcgcggg      480
68 cggccgagcc gaatccccct caccgggacg ccccgcctgc gctcgggaag aggcggggccc      540
70 tgcgcgccct gcgctcgcca tggcggtttg ggcggcgacg tgagcggctc cgcggacccc      600
72 gagcggggcc ccggccgcga cctgagccgc cgccgagcgc ccggggcc atg cga ccg      657
73                                     Met Arg Pro
74                                     1
76 acg ctg ctg tgg tgc ctg ctg ctg ctg ctc gga gtc ttc gcc gcc gcc      705
77 Thr Leu Leu Trp Ser Leu Leu Leu Leu Gly Val Phe Ala Ala Ala
78      5              10              15

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80	gcc gcg gcc ccg cca gac cct ctt tcc cag ctg ccc gct cct cag cac	753
81	Ala Ala Ala Pro Pro Asp Pro Leu Ser Gln Leu Pro Ala Pro Gln His	
82	20 25 30 35	
84	ccg aag att cgc ctg tac aac gca gag cag gtc ctg agt tgg gag cca	801
85	Pro Lys Ile Arg Leu Tyr Asn Ala Glu Gln Val Leu Ser Trp Glu Pro	
86	40 45 50	
88	gtg gcc ctg agc aat agc acg agg cct gtt gtc tac cga gtg cag ttt	849
89	Val Ala Leu Ser Asn Ser Thr Arg Pro Val Val Tyr Arg Val Gln Phe	
90	55 60 65	
92	aaa tac acc gac agt aaa tgg ttc acg gcc gac atc atg tcc ata ggg	897
93	Lys Tyr Thr Asp Ser Lys Trp Phe Thr Ala Asp Ile Met Ser Ile Gly	
94	70 75 80	
96	gtg aat tgt aca cag atc aca gca aca gag tgt gac ttc act gcc gcc	945
97	Val Asn Cys Thr Gln Ile Thr Ala Thr Glu Cys Asp Phe Thr Ala Ala	
98	85 90 95	
100	agt ccc tca gca ggc ttc cca atg gat ttc aat gtc act cta cgc ctt	993
101	Ser Pro Ser Ala Gly Phe Pro Met Asp Phe Asn Val Thr Leu Arg Leu	
102	100 105 110 115	
104	cga gct gag ctg gga gca ctc cat tct gcc tgg gtg aca atg cct tgg	1041
105	Arg Ala Glu Leu Gly Ala Leu His Ser Ala Trp Val Thr Met Pro Trp	
106	120 125 130	
108	ttt caa cac tat cgg aat gtg act gtc ggg cct cca gaa aac att gag	1089
109	Phe Gln His Tyr Arg Asn Val Thr Val Gly Pro Pro Glu Asn Ile Glu	
110	135 140 145	
112	gtg acc cca gga gaa ggc tcc ctc atc atc agg ttc tcc tct ccc ttt	1137
113	Val Thr Pro Gly Glu Gly Ser Leu Ile Ile Arg Phe Ser Ser Pro Phe	
114	150 155 160	
116	gac atc gct gat acc tcc acg gcc ttt ttt tgt tat tat gtc cat tac	1185
117	Asp Ile Ala Asp Thr Ser Thr Ala Phe Phe Cys Tyr Tyr Val His Tyr	
118	165 170 175	
120	tgg gaa aaa gga gga atc caa cag gtc aaa ggc cct ttc aga agc aac	1233
121	Trp Glu Lys Gly Gly Ile Gln Gln Val Lys Gly Pro Phe Arg Ser Asn	
122	180 185 190 195	
124	tcc att tca ttg gat aac tta aaa ccc tcc aga gtg tac tgt tta caa	1281
125	Ser Ile Ser Leu Asp Asn Leu Lys Pro Ser Arg Val Tyr Cys Leu Gln	
126	200 205 210	
128	gtc cag gca caa ctg ctt tgg aac aaa agt aac atc ttt aga gtc ggg	1329
129	Val Gln Ala Gln Leu Leu Trp Asn Lys Ser Asn Ile Phe Arg Val Gly	
130	215 220 225	
132	cat tta agc aac ata tct tgc tac gaa aca atg gca gat gcc tcc act	1377
133	His Leu Ser Asn Ile Ser Cys Tyr Glu Thr Met Ala Asp Ala Ser Thr	
134	230 235 240	
136	gag ctt cag caa gtc atc ctg atc tcc gtg gga aca ttt tcg ttg ctg	1425
137	Glu Leu Gln Gln Val Ile Leu Ile Ser Val Gly Thr Phe Ser Leu Leu	
138	245 250 255	
140	tcg gtg ctg gca gga gcc tgt ttc ttc ctg gtc ctg aaa tat aga ggc	1473
141	Ser Val Leu Ala Gly Ala Cys Phe Phe Leu Val Leu Lys Tyr Arg Gly	
142	260 265 270 275	
144	ctg att aaa tac tgg ttt cac act cca cca agc atc cca tta cag ata	1521

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```

145 Leu Ile Lys Tyr Trp Phe His Thr Pro Pro Ser Ile Pro Leu Gln Ile
146           280           285           290
148 gaa gag tat tta aaa gac cca act cag ccc atc tta gag gcc ttg gac 1569
149 Glu Glu Tyr Leu Lys Asp Pro Thr Gln Pro Ile Leu Glu Ala Leu Asp
150           295           300           305
152 aag gac agc tca cca aag gat gac gtc tgg gac tct gtg tcc att atc 1617
153 Lys Asp Ser Ser Pro Lys Asp Asp Val Trp Asp Ser Val Ser Ile Ile
154           310           315           320
156 tcg ttt ccg gaa aag gag caa gaa gat gtt ctc caa acg ctt tga 1662
157 Ser Phe Pro Glu Lys Glu Gln Glu Asp Val Leu Gln Thr Leu
158           325           330           335
160 accaaagcat gggcctagcc cactggctcc ctggaagaga tcaagccatc ggagctgcta 1722
162 gagttctgtc tggactttcc agagaccagt attccctttt gctgcctcta aaaggcctgt 1782
164 ccctgcagac atgagagaca gcagggtctca tgggggtgac aagctttttt tttttttct 1842
166 taaagaattt tcaaaatcaa attccagaat gattttacgg agatatccca ggaaaattaa 1902
168 ggcttctctt aaacactaaa aaggcatgta attgcttggt agcaaaatgg atatgacaca 1962
170 tctctgatac ttttttcatt attggttggg ctgagcagtc agaagacctg gtcgtcgtct 2022
172 tgacttttggc aaatgagccg gagcccttg ggcaggtcac acaacctgtc ccagcgaggg 2082
174 acactgagtg gcccttcatt tacatccatg gtgtgctggc ttaaaatgta attaattctg 2142
176 taaatatact cctagtaatt taagattttg tttttaaaact ggaaataaaa gattgtatag 2202
178 tgcattgttt tt 2214
181 <210> SEQ ID NO: 4
182 <211> LENGTH: 18
183 <212> TYPE: DNA
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
188 <223> OTHER INFORMATION: PCR Primer
190 <400> SEQUENCE: 4
191 cagcaggctt ccaatgg 18
194 <210> SEQ ID NO: 5
195 <211> LENGTH: 19
196 <212> TYPE: DNA
197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
201 <223> OTHER INFORMATION: PCR Primer
203 <400> SEQUENCE: 5
204 ggaggcccg cagtcacat 19
207 <210> SEQ ID NO: 6
208 <211> LENGTH: 28
209 <212> TYPE: DNA
210 <213> ORGANISM: Artificial Sequence
212 <220> FEATURE:
214 <223> OTHER INFORMATION: PCR Probe
216 <400> SEQUENCE: 6
217 tcaatgtcac tctacgcctt cgagctga 28
220 <210> SEQ ID NO: 7
221 <211> LENGTH: 19
222 <212> TYPE: DNA
223 <213> ORGANISM: Artificial Sequence

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225 <220> FEATURE:
227 <223> OTHER INFORMATION: PCR Primer
229 <400> SEQUENCE: 7
230 gaaggtgaag gtcggagtc 19
233 <210> SEQ ID NO: 8
234 <211> LENGTH: 20
235 <212> TYPE: DNA
236 <213> ORGANISM: Artificial Sequence
238 <220> FEATURE:
240 <223> OTHER INFORMATION: PCR Primer
242 <400> SEQUENCE: 8
243 gaagatggtg atgggatttc 20
246 <210> SEQ ID NO: 9
247 <211> LENGTH: 20
248 <212> TYPE: DNA
249 <213> ORGANISM: Artificial Sequence
251 <220> FEATURE:
253 <223> OTHER INFORMATION: PCR Probe
255 <400> SEQUENCE: 9
256 caagcttccc gttctcagcc 20
259 <210> SEQ ID NO: 10
260 <211> LENGTH: 339
261 <212> TYPE: DNA
262 <213> ORGANISM: Homo sapiens
264 <220> FEATURE:
266 <400> SEQUENCE: 10
267 ttttagtcga aatgtttgct ttaatagccc ccaaagtaca tattaagctt tcaactctcc 60
269 cccgcccccc tccccttttt tttgagacgg agtcaccagg ctggagtgca gtggggcgat 120
271 ctcggtcac tgcaacctcc gcctccagtc aacccattt tgaaaagggg ttttaaggga 180
273 aggagttaga aagggccagc tgaaggagga ggtggggctc tgggggtggg gggaatggcc 240
275 tccgagcagg gggagggaga gacagaaact tccagcattt ctaaattggc tggggtttgc 300
277 cctggagccg gcggcggtgc acgagtagga agtccttta 339
279 <210> SEQ ID NO: 11
280 <211> LENGTH: 54000
281 <212> TYPE: DNA
282 <213> ORGANISM: Homo sapiens
284 <220> FEATURE:
285 <221> NAME/KEY: exon
286 <222> LOCATION: (514)...(1420)
287 <223> OTHER INFORMATION: Exon 1
289 <221> NAME/KEY: intron
290 <222> LOCATION: (1421)...(12692)
291 <223> OTHER INFORMATION: Intron 1
293 <221> NAME/KEY: exon
294 <222> LOCATION: (12693)...(12825)
295 <223> OTHER INFORMATION: Exon 2
297 <221> NAME/KEY: intron
298 <222> LOCATION: (12826)...(19284)
299 <223> OTHER INFORMATION: Intron 2

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301 <221> NAME/KEY: exon
302 <222> LOCATION: (19285)...(19490)
303 <223> OTHER INFORMATION: Exon 3
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306 <222> LOCATION: (19491)...(24688)
307 <223> OTHER INFORMATION: Intron 3
309 <221> NAME/KEY: exon
310 <222> LOCATION: (24689)...(24837)
311 <223> OTHER INFORMATION: Exon 4
313 <221> NAME/KEY: intron
314 <222> LOCATION: (24838)...(29981)
315 <223> OTHER INFORMATION: Intron 4
317 <221> NAME/KEY: exon
318 <222> LOCATION: (29982)...(30141)
319 <223> OTHER INFORMATION: Exon 5
321 <221> NAME/KEY: intron
322 <222> LOCATION: (30142)...(30518)
323 <223> OTHER INFORMATION: Intron 5
325 <221> NAME/KEY: exon
326 <222> LOCATION: (30519)...(30676)
327 <223> OTHER INFORMATION: Exon 6
329 <221> NAME/KEY: intron
330 <222> LOCATION: (30677)...(34632)
331 <223> OTHER INFORMATION: Intron 6
333 <221> NAME/KEY: exon
334 <222> LOCATION: (34633)...(35318)
335 <223> OTHER INFORMATION: Exon 7
337 <400> SEQUENCE: 11
338 ggctggtctc caactoctgg cctcatgtga tccgccacc tcggcctcct aaagtgtga 60
339 gattacaggc gtgagccacc gcgcctggca tcagtgcata ctttttgaag tgattccaag 120
340 ttatcgcccg cttttttcgt gtaacatata aatacatctc tgtatctaga aatatccaat 180
341 gcataattca attgtctgcg aggtatttca tcacgtattt tcacgagcgt ggccaatttc 240
342 aaaatagttc tacaaagagg aaatgcaaga atgtgggaag agcaaaagaa aagctctatg 300
343 ttgcaaaacc catttttgct aacgtgtcca gtgggctccc gggacgacct gtttttaaat 360
344 tcttggtctc cctgcaccgc gtccctcctt tgetgcgcta gctttatgac gcactctgga 420
345 agaacagggc agatttaaaa ccctctccca acaggcgtca aacgacatgg tgcaggctcg 480
346 ggctggggag cgggcctgcg gctgcccagc tgctaaagga cttcctactc gtgcaccgcc 540
347 gccggctcca gggcaaacc caccgcatth agaaatgctg gaagtttctg tctctccctc 600
348 cccctgctcg gaggccattc cccccacccc cagagcccca cctcctcctt cactgggccc 660
349 tttctaactc cttcccctta aaaccctttt caaaatgggg ttgactggag gcgagggttg 720
350 cagtgaagcg agatcgcccc actgcactcc agcctggtga ctccgtctca aaaaaaagg 780
351 gaggggggcg ggggagagtt gaaagcttaa tatgtacttt gggggctatt aaagcaaaca 840
352 tttcgactaa aggggcgaat cctcgaattg tgcgatcaag caccgagag gagagtggg 900
353 gggggtcagg aggggtgggg gctccaggga aagcccgggg gtctgggccc ggggtctcgcg 960
354 gggcccttcc ggaaggatcg cggcccccga aggtgggctg ccgcgggggc tccagtctcc 1020
355 aggacgttcc gggaggctcc gcgctctggg aggcggctg cgtgggggtcc ccgcgctgca 1080
356 gccgcagagg cccccaggg ccgcggttcc cggagcggga aagtcccgcg cgggggcggt 1140
357 ggcctcgggg gcgggacggg gcgggggcgg gggcgcgggc ggccgagccg aatcccctcc 1200
358 accgggacgc cccgctgctg ctcgggaaga ggcgggccct gcgcgacctg cgctcgccat 1260

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/843,377

DATE: 05/14/2001

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Input Set : A:\RTS-0235 Sequence Listing.txt

Output Set: N:\CRF3\05142001\I843377.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date